

REPLACEMENT SHEET WITH MARKINGS

Fig. 1A

A

1 tgacttggatgtagacctcgaccttcacaggactcttcattgctggttggcaatg ATG TAT CGG CCA GAT GTG 73 ~~78~~
 1 M Y R P D V 6

74 GTG AGG GCT AGG AAA AGA GTT TGT TGG GAA CCC TGG GTT ATC GGC CTC GTC ATC TTC ATA 133 ~~78~~
 7 V R A R K R V C W E P W V I G L V I F I 26

134 TCC CTG ATT GTC CTG GCA GTG TGC ATT GGA CTC ACT GTT CAT TAT GTG AGA TAT AAT CAA 193 ~~78~~
 27 S L I V L A V C I G L T V H Y V R Y N Q 46

194 AAG AAG ACC TAC AAT TAC TAT AGC ACA TTG TCA TTT ACA ACT GAC AAA CTA TAT GCT GAG 253 ~~78~~
 47 K K T Y N Y Y S T L S F T T D K L Y A E 66

254 TTT GGC AGA GCT TCT AAC AAT TTT ACA GAA ATG AGC CAG AGA CTT GAA TCA ATG GTG 313 ~~78~~
 67 F G R E A S N N F T E M S Q R L E S M V 86

314 AAA AAT GCA TTT TAT AAA TCT CCA TTA AGG GAA TTT GTC AAG TCT CAG GTT ATC AAG 373 ~~78~~
 87 K N A F Y K S P L R E E F V K S Q V I K 106

374 TTC AGT CAA CAG AAG CAT GGA GTG TTG GCT CAT ATG CTG TTG ATT TGT AGA TTT CAC TCT 433 ~~78~~
 107 F S Q Q H G V L A H M L L I C R F H S 126

434 ACT GAG GAT CCT GAA ACT GTA GAT AAA ATT GTT CAA CTT GTT TTA CAT GAA AAG CTG CAA 493 ~~78~~
 127 T E D P E T V D K I V Q L V L H E K L Q 146

494 GAT GCT GTA GGA CCC CCT AAA GTA GAT CCT CAC TCA GTT AAA ATT AAA AAA ATC AAC AAG 553 ~~78~~
 147 D A V G P P K V D P H S V K I K K I N K 166

554 ACA GAA ACA GAC AGC TAT CTA AAC CAT TGC TGC GGA ACA CGA AGA AGT AAA ACT CTA GGT 613 ~~78~~
 167 T E T D S Y L N H C C G T R R S K T L G 186

614 CAG AGT CTC AGG ATC GTT GGT GGG ACA GAA GTA GAA GAG GGT GAA TGG CCC TGG CAG GCT 673 ~~78~~
 187 Q S L R I V G G T E V E E G E W P W Q A 206

674 AGC CTG CAG TGG GAT GGG AGT CAT CGC TGT GGA GCA ACC TTA ATT AAT GCC ACA TGG CTT 733 ~~78~~
 207 S L Q W D G S H R C G A T L I N A T W L 226

734 GTG AGT GCT GCT CAC TGT TTT ACA ACA TAT AAG AAC CCT GCC AGA TGG ACT GCT TCC TTT 793 ~~78~~
 227 V S A A H C F T T Y K N P A R W T A S F 246

794 GGA GTA ACA ATA AAA CCT TCG AAA ATG AAA CGG GGT CTC CGG AGA ATA ATT GTC CAT GAA 853 ~~78~~
 247 G V T I K P S K M K R G L R R I I V H E 266

854 AAA TAC AAA CAC CCA TCA CAT GAC TAT GAT ATT TCT CTT GCA GAG CTT TCT AGC CCT GTT 913 ~~78~~
 267 K Y K H P S H D Y D I S L A E L S S P V 286

914 CCC TAC ACA AAT GCA GTA CAT AGA GTT TGT CTC CCT GAT GCA TCC TAT GAG TTT CAA CCA 973 ~~78~~
 287 P Y T N A V H R V C L P D A S Y E F Q P 306

974 GGT GAT GTG ATG TTT GTG ACA GGA TTT GGA GCA CTG AAA AAT GAT GGT TAC AGT CAA AAT 1033 ~~78~~
 307 G D V M F V T G F G A L K N D G Y S Q N 326

1034 CAT CTT CGA CAA GCA CAG GTG ACT CTC ATA GAC GCT ACA ACT TGC AAT GAA CCT CAA GCT 1093 ~~78~~
 327 H L R Q A Q V T L I D A T T C N E P Q A 346

1094 TAC AAT GAC GCC ATA ACT CCT AGA ATG TTA TGT GCT GGC TCC TTA GAA GGA AAA ACA GAT 1153 ~~78~~
 347 Y N D A I T P R M L C A G S L E G K T D 366

1154 GCA TGC CAG GGT GAC TCT GGA GGA CCA CTG GTT AGT TCA GAT GCT AGA GAT ATC TGG TAC 1213 ~~78~~
 367 A C Q G D S G G P L V S S D A R D I W Y 386

1214 CTT GCT GGA ATA GTG AGC TGG GGA GAT GAA TGT GCG AAA CCC AAC AAG CCT GGT GTT TAT 1273 ~~78~~
 387 L A G I V S W G D E C A K P N K P G V Y 406

1274 ACT AGA GTT ACG GCC TTG CGG GAC TGG ATT ACT TCA AAA ACT GGT ATC TAA gagagaaaagcc 1336 ~~78~~
 407 T R V T A L R D W I T S K T G I * 423

1337 tcatggaacagataaacattttttttgttttttgggtgtggagccatttttagagatacagaattggagaagacttgca 1416

1417 aaacagctagatttgactgatctcaataaactgtttgcttgatgcaaaaaaaaaa 1471

REPLACEMENT SHEET WITH MARKINGS

Fig. 1B

1 tgacttgatgtagacctcgaccttcacaggactcttcattgctggttggaatg ATG TAT CGG CCA GAT GTG 73 ~~18~~
 1 M Y R P D V 6
 74 GTG AGG GCT AGG AAA AGA GTT TGT TGG GAA CCC TGG GTT ATC GGC CTC GTC ATG TTC ATA 133 ~~28~~
 7 V R A R K R V C W E P W V I G L V M F I 26
 134 TCC CTG ATT GTC CTG GCA GTG TGC ATT GGA GTC ACT GTT CAT TAT GTG AGA TAT AAT CAA 193 ~~38~~
 27 S L I V L A V C I G V T V H Y V R Y N Q 46
 194 AAG AAG ACC TAC AAT TAC TAT AGC ACA TTG TCA TTT ACA ACT GAC AAA CTA TAT GCT GAG 253 ~~48~~
 47 K K T Y N Y Y S T L S F T T D K L Y A E 66
 254 TTT GGC AGA GAG GCT TCT AAC AAT TTT ACA GAA ATG AGC CAG AGA CTT GAA TCA ATG GTG 313 ~~58~~
 67 F G R E A S N N F T E M S Q R L E S M V 86
 314 AAA AAT GCA TTT TAT AAA TCT CCA TTA AGG GAA GAA TTT GTC AAG TCT CAG GTT ATC AAG 373 ~~68~~
 87 K N A F Y K S P L R E E F V K S Q V I K 106
 374 TTC AGT CAA CAG AAG CAT GGA GTG TTG GCT CAT ATG CTG TTG ATT TGT AGA TTT CAC TCT 433 ~~78~~
 107 F S Q Q K H G V L A H M L L I C R F H S 126
 434 ACT GAG GAT CCT GAA ACT GTA GAT AAA ATT GTT CAA CTT GTT TTA CAT GAA AAG CTG CAA 493 ~~88~~
 127 T E D P E T V D K I V Q L V L H E K L Q 146
 494 GAT GCT GTA GGA CCC CCT AAA GTA GAT CCT CAC TCA GTT AAA ATT AAA AAA ATC AAC AAG 553 ~~98~~
 147 D A V G P P K V D P H S V K I K K I N K 166
 554 ACA GAA ACA GAC AGC TAT CTA AAC CAT TGC TGC GGA ACA CGA AGA AGT AAA ACT CTA GGT 613 ~~108~~
 167 T E T D S Y L N H C C G T R R S K T L G 186
 614 CAG AGT CTC AGG ATC GTT GGT GGG ACA GAA GTA GAA GAG GGT GAA TGG CCC TGG CAG GCT 673 ~~118~~
 187 Q S L R A I V G G T E V E E G E W P W Q A 206
 674 AGC CTG CAG TGG GAT GGG AGT CAT CGC TGT GGA GCA ACC TTA ATT AAT GCC ACA TGG CTT 733 ~~128~~
 207 S L Q W D G S H R C G A T L I N A T W L 226
 734 GTG AGT GCT GCT CAC TGT TTT ACA ACA TAT AAG AAC CCT GCC AGA TGG ACT GCT TCC TTT 793 ~~138~~
 227 V S A A H C F T T Y K N P A R W T A S F 246
 794 GGA GTA ACA ATA AAA CCT TCG AAA ATG AAA CGG GGT CTC CGG AGA ATA ATT GTC CAT GAA 853 ~~148~~
 247 G V T I K P S K M K R G L R R I I V H E 266
 854 AAA TAC AAA CAC CCA TCA CAT GAC TAT GAT ATT TCT CTT GCA GAG CTT TCT AGC CCT GTT 913 ~~158~~
 267 K Y K H P S H D Y D I S L A E L S S P V 286
 914 CCC TAC ACA AAT GCA GTA CAT AGA GTT TGT CTC CCT GAT GCA TCC TAT GAG TTT CAA CCA 973 ~~168~~
 287 P Y T N A V H R V C L P D A S Y E F Q P 306
 974 GGT GAT GTG ATG TTT GTG ACA GGA TTT GGA GCA CTG AAA AAT GAT GGT TAC AGT CAA AAT 1033 ~~178~~
 307 G D V M F V T G F G A L K N D G Y S Q N 326
 1034 CAT CTT CGA CAA GCA CAG GTG ACT CTC ATA GAC GCT ACA ACT TGC AAT GAA CCT CAA GCT 1093 ~~188~~
 327 H L R Q A Q V T L I D A T T C N E P Q A 346
 1094 TAC AAT GAC GCC ATA ACT CCT AGA ATG TTA TGT GCT GGC TCC TTA GAA GGA AAA ACA GAT 1153 ~~198~~
 347 Y N D A I T P R M L C A G S L E G K T D 366
 1154 GCA TGC CAG GGT GAC TCT GGA GGA CCA CTG GTT AGT TCA GAT GAT AGA GAT ATC TGG TAC 1213 ~~208~~
 367 A C Q G D S G G P L V S S D A R D I W Y 386
 1214 CTT GCT GGA ATA GAG AGC TGG GGA GAT GAA TGT GCG AAA CCC AAC AAG CCT GGT GTT TAT 1273 ~~218~~
 387 L A G I V S S G D E C A K P N K P G V Y 406
 1274 ACT AGA GTT ACG GCC TTG CGG GAC TGG ATT ACT TCA AAA ACT GGT ATC TAA gagagaaaagcc 1336 ~~228~~
 407 T R V T A L R D W I T S K T G I * 423
 1337 tcatggaacagataacatTTTTTTTTTgTTTTTgggtgtggagccatttttagagatacagaattggagaagacttgca 1416
 1417 aaacagctagatttgactgatctcaataaactgtttgcttgatgcaaaaaaaaaa 1471

REPLACEMENT SHEET WITH MARKINGS

Fig. 1B (con't)

A

1 tgacttgatgtagacctcgaccttcacaggactcttcattgctggttggaatg ATG TAT CGG CCA GAT GTG 73
 1 M Y R P D V 6
 74 GTG AGG GCT AGG AAA AGA GTT TGT TGG GAA CCC TGG GTT ATC GGC CTC GTC ATG TTC ATA 133
 7 V R A R K R V C W E P W V I G L V M F I 26
 134 TCC CTG ATT GTC CTG GCA GTG TGC ATT GGA GTC ACT GTT CAT TAT GTG AGA TAT AAT CAA 193
 27 S L I V L A V C I G V T V H Y V R Y N Q 46
 194 AAG AAG ACC TAC AAT TAC TAT AGC ACA TTG TCA TTT ACA ACT GAC AAA CTA TAT GCT GAG 253
 47 K K T Y N Y Y S T L S F T T D K L Y A E 66
 254 TTT GGC AGA GAG GCT TCT AAC AAT TTT ACA GAA ATG AGC CAG AGA CTT GAA TCA ATG GTG 313
 67 F G R E A S N N F T E M S Q R L E S M V 86
 314 AAA AAT GCA TTT TAT AAA TCT CCA TTA AGG GAA GAA TTT GTC AAG TCT CAG GTT ATC AAG 373
 87 K N A F Y K S P L R E E F V K S Q V I K 106
 374 TTC AGT CAA CAG AAG CAT GGA GTG TTG GCT CAT ATG CTG TTG ATT TGT AGA TTT CAC TCT 433
 107 F S Q Q K H G V L A H M L L I C R F H S 126
 434 ACT GAG GAT CCT GAA ACT GTA GAT AAA ATT GTT CAA CTT GTT TTA CAT GAA AAG CTG CAA 493
 127 T E D P E T V D K I V Q L V L H E K L Q 146
 494 GAT GCT GTA GGA CCC CCT AAA GTA GAT CCT CAC TCA GTT AAA ATT AAA AAA ATC AAC AAG 553
 147 D A V G P P K V D P H S V K I K K I N K 166
 554 ACA GAA ACA GAC AGC TAT CTA AAC CAT TGC TGC GGA ACA CGA AGA AGT AAA ACT CTA GGT 613
 167 T E T D S Y L N H C C G T R R S K T L G 186
 614 CAG AGT CTC AGG ATC GTT GGT GGG ACA GAA GTA GAA GAG GGT GAA TGG CCC TGG CAG GCT 673
 187 Q S L R A I V G G T E V E E G E W P W Q A 206
 674 AGC CTG CAG TGG GAT GGG AGT CAT CGC TGT GGA GCA ACC TTA ATT AAT GCC ACA TGG CTT 733
 207 S L Q W D G S H R C G A T L I N A T W L 226
 734 GTG AGT GCT GCT CAC TGT TTT ACA ACA TAT AAG AAC CCT GCC AGA TGG ACT GCT TCC TTT 793
 227 V S A A H C F T T Y K N P A R W T A S F 246
 794 GGA GTA ACA ATA AAA CCT TCG AAA ATG AAA CGG GGT CTC CGG AGA ATA ATT GTC CAT GAA 853
 247 G V T I K P S K M K R G L R R I I V H E 266
 854 AAA TAC AAA CAC CCA TCA CAT GAC TAT GAT ATT TCT CTT GCA GAG CTT TCT AGC CCT GTT 913
 267 K Y K H P S H D Y D I S L A E L S S P V 286
 914 CCC TAC ACA AAT GCA GTA CAT AGA GTT TGT CTC CCT GAT GCA TCC TAT GAG TTT CAA CCA 973
 287 P Y T N A V H R V C L P D A S Y E F Q P 306
 974 GGT GAT GTG ATG TTT GTG ACA GGA TTT GGA GCA CTG AAA AAT GAT GGT TAC AGT CAA AAT 1033
 307 G D V M F V T G F G A L K N D G Y S Q N 326
 1034 CAT CTT CGA CAA GCA CAG GTG ACT CTC ATA GAC GCT ACA ACT TGC AAT GAA CCT CAA GCT 1093
 327 H L R Q A Q V T L I D A T T C N E P Q A 346
 1094 TAC AAT GAC GCC ATA ACT CCT AGA ATG TTA TGT GCT GSC TCC TTA GAA GGA AAA ACA GAT 1153
 347 Y N D A I T P R M L C A G S L E G K T D 366
 1154 GCA TGC CAG GGT GAC TCT GGA GGA CCA CTG GTT AGT TCA GAT GCT AGA GAT ATC TGG TAC 1213
 367 A C Q G D S G G P L V S S D A R D I W Y 386
 1214 CTT GCT GGA ATA GTG AGC TCG GGA GAT GAA TGT GCG AAA CCC AAC AAG CCT GGT GTT TAT 1273
 387 L A G I V S S G D E C A K P N K P G V Y 406
 1274 ACT AGA GTT ACG GCC TTG CGG GAC TGG ATT ACT TCA AAA ACT GGT ATC TAA gagagaaaagcc 1336
 407 T R V T A L R D W I T S K T G I * 423
 1337 tcatggaacagataaacattttttttgttttttgggtgtggaggccatttttagagatacagaattggagaagacttgca 1416
 1417 aaacagctagatttgactgatctcataaactgtttgttgatgcaaaaaaaaaa 1471